

# SEQUENCE LISTING

<110> Brzostowicz, Patricia C.  
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Rouviere, Pierre E.

<120> CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

<130> CL1903 US NA

<150> 60/229,907

<151> 2000-09-01

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<160> 60

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<212> DNA

<213> Methylomonas 16a

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<213> Methylomonas 16a

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Lys Lys Val Ala Ile Leu Thr Ala Gly Gly Leu Ala Pro Cys Leu Asn  
 35 40 45

Ser Ala Ile Gly Ser Leu Ile Glu Arg Tyr Thr Glu Ile Asp Pro Ser  
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Ile Glu Ile Ile Cys Tyr Arg Gly Gly Tyr Lys Gly Leu Leu Leu Gly  
 65 70 75 80

Asp Ser Tyr Pro Val Thr Ala Glu Val Arg Lys Lys Ala Gly Val Leu  
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Gln Arg Phe Gly Gly Ser Val Ile Gly Asn Ser Arg Val Lys Leu Thr  
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 Asn Val Lys Asp Cys Val Lys Arg Gly Leu Val Lys Glu Gly Glu Asp  
 115 120 125  
 Pro Gln Lys Val Ala Ala Asp Gln Leu Val Lys Asp Gly Val Asp Ile  
 130 135 140  
 Leu His Thr Ile Gly Gly Asp Asp Thr Asn Thr Ala Ala Ala Asp Leu  
 145 150 155 160  
 Ala Ala Phe Leu Ala Arg Asn Asn Tyr Gly Leu Thr Val Ile Gly Leu  
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 Pro Lys Thr Val Asp Asn Asp Val Phe Pro Ile Lys Gln Ser Leu Gly  
 180 185 190  
 Ala Trp Thr Ala Ala Glu Gln Gly Ala Arg Tyr Phe Met Asn Val Val  
 195 200 205  
 Ala Glu Asn Asn Ala Asn Pro Arg Met Leu Ile Val His Glu Val Met  
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 Gly Arg Asn Cys Gly Trp Leu Thr Ala Ala Thr Ala Gln Glu Tyr Arg  
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 Lys Leu Leu Asp Arg Ala Glu Trp Leu Pro Glu Leu Gly Leu Thr Arg  
 245 250 255  
 Glu Ser Tyr Glu Val His Ala Val Phe Val Pro Glu Met Ala Ile Asp  
 260 265 270  
 Leu Glu Ala Glu Ala Lys Arg Leu Arg Glu Val Met Asp Lys Val Asp  
 275 280 285  
 Cys Val Asn Ile Phe Val Ser Glu Gly Ala Gly Val Glu Ala Ile Val  
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 Ala Glu Met Gln Ala Lys Gly Gln Glu Val Pro Arg Asp Ala Phe Gly  
 305 310 315 320  
 His Ile Lys Leu Asp Ala Val Asn Pro Gly Lys Trp Phe Gly Glu Gln  
 325 330 335  
 Phe Ala Gln Met Ile Gly Ala Glu Lys Thr Leu Val Gln Lys Ser Gly  
 340 345 350

Tyr Phe Ala Arg Ala Ser Ala Ser Asn Val Asp Asp Met Arg Leu Ile  
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Lys Ser Cys Ala Asp Leu Ala Val Glu Cys Ala Phe Arg Arg Glu Ser  
 370 375 380

Gly Val Ile Gly His Asp Glu Asp Asn Gly Asn Val Leu Arg Ala Ile  
 385 390 395 400

Glu Phe Pro Arg Ile Lys Gly Gly Lys Pro Phe Asn Ile Asp Thr Asp  
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Val Glu Val Ser His  
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- <213> Methylomonas 16a

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<212> PRT

<213> Methylomonas 16a

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Ala Arg Ala Leu Val Asp Gly Gly Leu Lys Val Leu Glu Ile Thr Leu  
35 40 45

Arg Thr Pro Val Ala Leu Glu Cys Ile Arg Arg Ile Lys Ala Glu Val  
50 55 60

Pro Asp Ala Ile Val Gly Ala Gly Thr Ile Ile Asn Pro His Thr Leu  
65 70 75 80

Tyr Gln Ala Ile Asp Ala Gly Ala Glu Phe Ile Val Ser Pro Gly Ile  
85 90 95

Thr Glu Asn Leu Leu Asn Glu Ala Leu Ala Ser Gly Val Pro Ile Leu  
100 105 110

Pro Gly Val Ile Thr Pro Ser Glu Val Met Arg Leu Leu Glu Lys Gly  
115 120 125

Ile Asn Ala Met Lys Phe Phe Pro Ala Glu Ala Ala Gly Gly Ile Pro  
130 135 140

Met Leu Lys Ser Leu Gly Gly Pro Leu Pro Gln Val Thr Phe Cys Pro  
145 150 155 160

Thr Gly Gly Val Asn Pro Lys Asn Ala Pro Glu Tyr Leu Ala Leu Lys  
165 170 175

Asn Val Ala Cys Val Gly Gly Ser Trp Met Ala Pro Ala Asp Leu Val  
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Asp Ala Glu Asp Trp Ala Glu Ile Thr Arg Arg Ala Ser Glu Ala Ala  
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Ala Leu Lys Lys  
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<212> PRT

<213> Methylomonas 16a

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Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His  
 35 40 45

Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr  
 50 55 60

Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln  
 65 70 75 80

Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr  
 85 90 95

Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser  
 100 105 110

Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala  
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Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys  
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Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr  
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Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile  
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Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn  
180 185 190

Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg  
195 200 205

Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu  
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Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr  
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Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His  
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Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr  
260 265 270

Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala  
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Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp  
290 295 300

Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr  
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Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp  
325 330 335

Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu  
340 345 350

Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile  
355 360 365

Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly  
370 375 380

Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr  
385 390 395 400

Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe  
405 410 415

Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala  
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Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile  
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Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly  
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Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly  
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Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys  
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Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly  
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Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr  
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Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu  
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Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val  
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Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln  
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Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val  
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<212> DNA

<213> Methylomonas 16a

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<212> PRT

<213> Methylomonas 16a

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Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala  
35 40 45

His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu  
50 55 60

Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu  
 65 70 75 80  
 Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp  
 85 90 95  
 Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu  
 100 105 110  
 Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala  
 115 120 125  
 Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly  
 130 135 140  
 Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys  
 145 150 155 160  
 Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg  
 165 170 175  
 Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu  
 180 185 190  
 Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp  
 195 200 205  
 Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys  
 210 215 220  
 Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp  
 225 230 235 240  
 Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val  
 245 250 255  
 Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met  
 260 265 270  
 Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser  
 275 280 285  
 Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu  
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 Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala  
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Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu  
 325 330 335

Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe Thr Asp Ile  
 340 345 350

Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala  
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<213> Methylomonas 16a

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35 40 45

Ala Phe Gln Lys Val Ala Val Ala Ile Ser Val Glu Asp Pro Tyr Trp  
50 55 60

Pro Glu Leu Ser Ile Ala Lys His Pro Asp Ile Ile Thr Ala Pro Gly  
65 70 75 80

Gly Lys Glu Arg Ala Asp Ser Val Leu Ser Ala Leu Lys Ala Leu Glu  
85 90 95

Asp Ile Ala Ser Glu Asn Asp Trp Val Leu Val His Asp Ala Ala Arg  
100 105 110

Pro Cys Leu Thr Gly Ser Asp Ile His Leu Gln Ile Asp Thr Leu Lys  
115 120 125

Asn Asp Pro Val Gly Gly Ile Leu Ala Leu Ser Ser His Asp Thr Leu  
130 135 140

Lys His Val Asp Gly Asp Thr Ile Thr Ala Thr Ile Asp Arg Lys His  
145 150 155 160

Val Trp Arg Ala Leu Thr Pro Gln Met Phe Lys Tyr Gly Met Leu Arg  
165 170 175

Asp Ala Leu Gln Arg Thr Glu Gly Asn Pro Ala Val Thr Asp Glu Ala  
180 185 190

Ser Ala Leu Glu Leu Leu Gly His Lys Pro Lys Ile Val Glu Gly Arg  
195 200 205

Pro Asp Asn Ile Lys Ile Thr Arg Pro Glu Asp Leu Ala Leu Ala Gln  
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Phe Tyr Met Glu Gln Gln Ala  
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<210> 11

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<212> DNA

<213> Methylomonas 16a

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<211> 285

<212> PRT

<213> Methylomonas 16a

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Leu Leu Gln Thr Val Phe Gln Met Leu Asp Leu Cys Asp Trp Leu Thr  
 35 40 45  
 Phe His Pro Val Asp Asp Gly Arg Val Thr Leu Arg Asn Pro Ile Ser  
 50 55 60  
 Gly Val Pro Glu Gln Asp Asp Leu Thr Val Arg Ala Ala Asn Leu Leu  
 65 70 75 80  
 Lys Ser His Thr Gly Cys Val Arg Gly Val Cys Ile Asp Ile Glu Lys  
 85 90 95  
 Asn Leu Pro Met Gly Gly Gly Leu Gly Gly Gly Ser Ser Asp Ala Ala  
 100 105 110  
 Thr Thr Leu Val Val Leu Asn Arg Leu Trp Gly Leu Gly Leu Ser Lys  
 115 120 125  
 Arg Glu Leu Met Asp Leu Gly Leu Arg Leu Gly Ala Asp Val Pro Val  
 130 135 140  
 Phe Val Phe Gly Cys Ser Ala Trp Gly Glu Gly Val Ser Glu Asp Leu  
 145 150 155 160  
 Gln Ala Ile Thr Leu Pro Glu Gln Trp Phe Val Ile Ile Lys Pro Asp  
 165 170 175  
 Cys His Val Asn Thr Gly Glu Ile Phe Ser Ala Glu Asn Leu Thr Arg  
 180 185 190  
 Asn Ser Ala Val Val Thr Met Ser Asp Phe Leu Ala Gly Asp Asn Arg  
 195 200 205  
 Asn Asp Cys Ser Glu Val Val Cys Lys Leu Tyr Arg Pro Val Lys Asp  
 210 215 220  
 Ala Ile Asp Ala Leu Leu Cys Tyr Ala Glu Ala Arg Leu Thr Gly Thr  
 225 230 235 240  
 Gly Ala Cys Val Phe Ala Gln Phe Cys Asn Lys Glu Asp Ala Glu Ser  
 245 250 255  
 Ala Leu Glu Gly Leu Lys Asp Arg Trp Leu Val Phe Leu Ala Lys Gly  
 260 265 270  
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 275 280 285

<210> 13  
 <211> 471  
 <212> DNA  
 <213> Methylomonas 16a

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 gtgtgcacg cattggccga cgccatcttg ggagccgcg ctttgggcga catcggcaaa 180  
 catttcccgg acaccgaccc caatttcaag ggcgccgaca gcaggggtgt actgcgccac 240  
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 gctcaggcgc cgaagatgct gccacacgtg cccggcatgc gcgccaacat tgccgccgat 360  
 ctggaaaccg atgtcgattt cattaatgta aaagccacga cgaccgagaa actgggcttt 420  
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<210> 14  
 <211> 157  
 <212> PRT  
 <213> Methylomonas 16a

<400> 14  
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 Asp His Ile Ile Leu Gly Gly Val Lys Ile Pro Tyr Glu Lys Gly Leu  
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 Glu Ala His Ser Asp Gly Asp Val Val Leu His Ala Leu Ala Asp Ala  
 35 40 45  
 Ile Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys His Phe Pro Asp  
 50 55 60  
 Thr Asp Pro Asn Phe Lys Gly Ala Asp Ser Arg Val Leu Leu Arg His  
 65 70 75 80  
 Val Tyr Gly Ile Val Lys Glu Lys Gly Tyr Lys Leu Val Asn Ala Asp  
 85 90 95



Val Thr Ile Ile Ala Gln Ala Pro Lys Met Leu Pro His Val Pro Gly  
 100 105 110

Met Arg Ala Asn Ile Ala Ala Asp Leu Glu Thr Asp Val Asp Phe Ile  
 115 120 125

Asn Val Lys Ala Thr Thr Thr Glu Lys Leu Gly Phe Glu Gly Arg Lys  
 130 135 140

Glu Gly Ile Ala Val Gln Ala Val Val Leu Ile Glu Arg  
 145 150 155

<210> 15

<211> 1632

<212> DNA

<213> Methylomonas 16a

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 gtgaccgaag acggtgccga aaccgatttg gaccttggcc attacgaacg gtttttgaaa 240  
 accacgatga ccaagaaaaa caacttcacc accggtcagg tttacgagca ggtattacgc 300  
 aacgagcgca aaggtgatta tcttggcgcg accgtgcaag tcattccaca tatcaccgac 360  
 gaaatcaaac gccgggtgta tgaaagcgcc gaagggaaaag atgtggcatt gatcgaagtc 420  
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 gggattcagc cggacatttt gatctgtcgt tcagaacaac cgatcccggc cagtgaacgc 660  
 cgcaagatcg cgctatttac caatgtcgcc gaaaaggcgg tgatttccgc gatcgatgcc 720  
 gacaccattt accgcattcc gctattgctg cgcgaacaag gcctggacga cctggtggtc 780  
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 accgaattcc tgccgaaatc gccacaccct gtgatcggct tgatcaccga atggatggac 1260  
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 gagctaccg aacaccctg gttcctggcc tgccagttcc atcccgaatt cacctcgacg 1560  
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 caaggcacag ca 1632

<210> 16

<211> 544

<212> PRT

<213> Methylomonas 16a

<400> 16

Met Thr Lys Phe Ile Phe Ile Thr Gly Gly Val Val Ser Ser Leu Gly  
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Lys Gly Ile Ala Ala Ser Ser Leu Ala Ala Ile Leu Glu Asp Arg Gly  
 20 25 30

Leu Lys Val Thr Ile Thr Lys Leu Asp Pro Tyr Ile Asn Val Asp Pro  
 35 40 45

Gly Thr Met Ser Pro Phe Gln His Gly Glu Val Phe Val Thr Glu Asp  
 50 55 60

Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg Phe Leu Lys  
 65 70 75 80

Thr Thr Met Thr Lys Lys Asn Asn Phe Thr Thr Gly Gln Val Tyr Glu  
 85 90 95

Gln Val Leu Arg Asn Glu Arg Lys Gly Asp Tyr Leu Gly Ala Thr Val  
 100 105 110

Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Arg Arg Val Tyr Glu  
 115 120 125

Ser Ala Glu Gly Lys Asp Val Ala Leu Ile Glu Val Gly Gly Thr Val  
130 135 140

Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Thr Ile Arg Gln Met Gly  
145 150 155 160

Val Glu Leu Gly Arg Asp Arg Ala Leu Phe Ile His Leu Thr Leu Val  
165 170 175

Pro Tyr Ile Lys Ser Ala Gly Glu Leu Lys Thr Lys Pro Thr Gln His  
180 185 190

Ser Val Lys Glu Leu Arg Thr Ile Gly Ile Gln Pro Asp Ile Leu Ile  
195 200 205

Cys Arg Ser Glu Gln Pro Ile Pro Ala Ser Glu Arg Arg Lys Ile Ala  
210 215 220

Leu Phe Thr Asn Val Ala Glu Lys Ala Val Ile Ser Ala Ile Asp Ala  
225 230 235 240

Asp Thr Ile Tyr Arg Ile Pro Leu Leu Leu Arg Glu Gln Gly Leu Asp  
245 250 255

Asp Leu Val Val Asp Gln Leu Arg Leu Asp Val Pro Ala Ala Asp Leu  
260 265 270

Ser Ala Trp Glu Lys Val Val Asp Gly Leu Thr His Pro Thr Asp Glu  
275 280 285

Val Ser Ile Ala Ile Val Gly Lys Tyr Val Asp His Thr Asp Ala Tyr  
290 295 300

Lys Ser Leu Asn Glu Ala Leu Ile His Ala Gly Ile His Thr Arg His  
305 310 315 320

Lys Val Gln Ile Ser Tyr Ile Asp Ser Glu Thr Ile Glu Ala Glu Gly  
325 330 335

Thr Ala Lys Leu Lys Asn Val Asp Ala Ile Leu Val Pro Gly Gly Phe  
340 345 350

Gly Glu Arg Gly Val Glu Gly Lys Ile Ser Thr Val Arg Phe Ala Arg  
355 360 365

Glu Asn Lys Ile Pro Tyr Leu Gly Ile Cys Leu Gly Met Gln Ser Ala  
370 375 380

Val Ile Glu Phe Ala Arg Asn Val Val Gly Leu Glu Gly Ala His Ser  
385 390 395 400

Thr Glu Phe Leu Pro Lys Ser Pro His Pro Val Ile Gly Leu Ile Thr  
405 410 415

Glu Trp Met Asp Glu Ala Gly Glu Leu Val Thr Arg Asp Glu Asp Ser  
420 425 430

Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Gln Lys Cys Arg Leu Lys  
435 440 445

Ala Asp Ser Leu Ala Phe Gln Leu Tyr Gln Lys Asp Val Ile Thr Glu  
450 455 460

Arg His Arg His Arg Tyr Glu Phe Asn Asn Gln Tyr Leu Lys Gln Leu  
465 470 475 480

Glu Ala Ala Gly Met Lys Phe Ser Gly Lys Ser Leu Asp Gly Arg Leu  
485 490 495

Val Glu Ile Ile Glu Leu Pro Glu His Pro Trp Phe Leu Ala Cys Gln  
500 505 510

Phe His Pro Glu Phe Thr Ser Thr Pro Arg Asn Gly His Ala Leu Phe  
515 520 525

Ser Gly Phe Val Glu Ala Ala Ala Lys His Lys Thr Gln Gly Thr Ala  
530 535 540

<210> 17

<211> 954

<212> DNA

<213> Methylomonas 16a

<400> 17

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cataac	cgca	ccgtgg	tcga	tggact	gaaa	caaaa	aggtg	cggtgt	tcac	cgagga	acta	180
agcgat	gtgc	cggtgg	gttc	ctactt	gatt	ttcagc	gcgc	acggcg	tatc	caaggag	gtg	240
caacag	gaag	ccgagg	agcg	ccagtt	gacg	gtattc	gatg	cgactt	gtcc	gctggg	tacc	300
aaagtgc	caca	tgcagg	ttgc	caagcat	gcc	aaacagg	ggcc	gagaagt	gat	tttgat	cggc	360

cacgccgggtc atccggaagt ggaaggcacg atggggccagt atgaaaaatg caccgaaggc 420  
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 aatgatctgg cctatgtgac gcagacgacc ttgtcgatga cgcacaccaa ggatcatgggtg 540  
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 atcgatcaac tgaaggcatg ggcggcgcaa accacttcgg tcagagaaaa cagcggcatc 900  
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<210> 18

<211> 318

<212> PRT

<213> Methylomonas 16a

<400> 18

Met Gln Ile Val Leu Ala Asn Pro Arg Gly Phe Cys Ala Gly Val Asp  
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Arg Ala Ile Glu Ile Val Asp Gln Ala Ile Glu Ala Phe Gly Ala Pro  
20 25 30

Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly  
35 40 45

Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro  
50 55 60

Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val  
65 70 75 80

Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys  
85 90 95

Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln  
100 105 110

Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu  
115 120 125

Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Gly Ile Tyr  
130 135 140

Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro  
145 150 155 160

Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr  
165 170 175

Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu  
180 185 190

Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala  
195 200 205

Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser  
210 215 220

Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu  
225 230 235 240

Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp  
245 250 255

Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala  
260 265 270

Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly  
275 280 285

Gly Glu Thr Thr Ser Val Arg Glu Asn Ser Gly Ile Glu Glu Lys Val  
290 295 300

Val Phe Ser Ile Pro Lys Glu Leu Lys Lys His Met Gln Ala  
305 310 315

<210> 19

<211> 891

<212> DNA

<213> Methylomonas 16a

<400> 19

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gtattgaacg gcggaacg caccggccc ttgttgactt atgcgaccgg tcaggctttg 180  
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tcgctgattc acgacgatct gccggccatg gacaacgatg atctgcgcgg cggcaaacg 300  
acctgtcaca aggcttacga cgaggccacc gccatttttg ccggcgacgc actgcaggcg 360  
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aaaatgatca cggctttgac ccgcgccagc ggctctcaag gcatggggg cggtaagcc 480  
atcgatctcg gctccgctcg ccgcaaattg acgctgcgg aactcgaaaa catgcatatc 540  
cacaagactg gcgccctgat ccgcgccagc gtcaatctgg cggcattatc caaacccgat 600  
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caggtcaaag acgacattct cgacatcgaa gccgacaccg cgacactcgg caagactcag 720  
ggcaaggaca tcgataacga caaacgacc taccctgcgc tattgggcat ggctggcgcc 780  
aaacaaaaag cccaggaatt gcacgaacaa gcagtcgaaa gcttaacggg atttggcagc 840  
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<210> 20

<211> 297

<212> PRT

<213> Methylomonas 16a

<400> 20

Met Ser Lys Leu Lys Ala Tyr Leu Thr Val Cys Gln Glu Arg Val Glu  
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Arg Ala Leu Asp Ala Arg Leu Pro Ala Glu Asn Ile Leu Pro Gln Thr  
20 25 30

Leu His Gln Ala Met Arg Tyr Ser Val Leu Asn Gly Gly Lys Arg Thr  
35 40 45

Arg Pro Leu Leu Thr Tyr Ala Thr Gly Gln Ala Leu Gly Leu Pro Glu  
50 55 60

Asn Val Leu Asp Ala Pro Ala Cys Ala Val Glu Phe Ile His Val Tyr  
65 70 75 80

Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp Leu Arg  
85 90 95

Arg Gly Lys Pro Thr Cys His Lys Ala Tyr Asp Glu Ala Thr Ala Ile  
100 105 110

Leu Ala Gly Asp Ala Leu Gln Ala Leu Ala Phe Glu Val Leu Ala Asn  
115 120 125

Asp Pro Gly Ile Thr Val Asp Ala Pro Ala Arg Leu Lys Met Ile Thr  
130 135 140

Ala Leu Thr Arg Ala Ser Gly Ser Gln Gly Met Val Gly Gly Gln Ala  
145 150 155 160

Ile Asp Leu Gly Ser Val Gly Arg Lys Leu Thr Leu Pro Glu Leu Glu  
165 170 175

Asn Met His Ile His Lys Thr Gly Ala Leu Ile Arg Ala Ser Val Asn  
180 185 190

Leu Ala Ala Leu Ser Lys Pro Asp Leu Asp Thr Cys Val Ala Lys Lys  
195 200 205

Leu Asp His Tyr Ala Lys Cys Ile Gly Leu Ser Phe Gln Val Lys Asp  
210 215 220

Asp Ile Leu Asp Ile Glu Ala Asp Thr Ala Thr Leu Gly Lys Thr Gln  
225 230 235 240

Gly Lys Asp Ile Asp Asn Asp Lys Pro Thr Tyr Pro Ala Leu Leu Gly  
245 250 255

Met Ala Gly Ala Lys Gln Lys Ala Gln Glu Leu His Glu Gln Ala Val  
260 265 270

Glu Ser Leu Thr Gly Phe Gly Ser Glu Ala Asp Leu Leu Arg Glu Leu  
275 280 285

Ser Leu Tyr Ile Ile Glu Arg Thr His  
290 295

<210> 21

<211> 1533

<212> DNA

<213> Methylomonas 16a

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<210> 22

<211> 511

<212> PRT

<213> *Methylobionas* 16a

<400> 22

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 Phe Asp Lys His Ala Glu Ile Gly Gly Arg Asn Arg Pro Ile Asn Met  
 35 40 45  
 Asn Gly Phe Thr Phe Asp Thr Gly Pro Thr Phe Leu Leu Met Lys Gly  
 50 55 60  
 Val Leu Asp Glu Met Phe Glu Leu Cys Glu Arg Arg Ser Glu Asp Tyr  
 65 70 75 80  
 Leu Glu Phe Leu Pro Leu Ser Pro Met Tyr Arg Leu Leu Tyr Asp Asp  
 85 90 95  
 Arg Asp Ile Phe Val Tyr Ser Asp Arg Glu Asn Met Arg Ala Glu Leu  
 100 105 110  
 Gln Arg Val Phe Asp Glu Gly Thr Asp Gly Tyr Glu Gln Phe Met Glu  
 115 120 125  
 Gln Glu Arg Lys Arg Phe Asn Ala Leu Tyr Pro Cys Ile Thr Arg Asp  
 130 135 140  
 Tyr Ser Ser Leu Lys Ser Phe Leu Ser Leu Asp Leu Ile Lys Ala Leu  
 145 150 155 160  
 Pro Trp Leu Ala Phe Pro Lys Ser Val Phe Asn Asn Leu Gly Gln Tyr  
 165 170 175  
 Phe Asn Gln Glu Lys Met Arg Leu Ala Phe Cys Phe Gln Ser Lys Tyr  
 180 185 190  
 Leu Gly Met Ser Pro Trp Glu Cys Pro Ala Leu Phe Thr Met Leu Pro  
 195 200 205  
 Tyr Leu Glu His Glu Tyr Gly Ile Tyr His Val Lys Gly Gly Leu Asn  
 210 215 220  
 Arg Ile Ala Ala Ala Met Ala Gln Val Ile Ala Glu Asn Gly Gly Glu  
 225 230 235 240  
 Ile His Leu Asn Ser Glu Ile Glu Ser Leu Ile Ile Glu Asn Gly Ala  
 245 250 255

Ala Lys Gly Val Lys Leu Gln His Gly Ala Glu Leu Arg Gly Asp Glu  
 260 265 270

Val Ile Ile Asn Ala Asp Phe Ala His Ala Met Thr His Leu Val Lys  
 275 280 285

Pro Gly Val Leu Lys Lys Tyr Thr Pro Glu Asn Leu Lys Gln Arg Glu  
 290 295 300

Tyr Ser Cys Ser Thr Phe Met Leu Tyr Leu Gly Leu Asp Lys Ile Tyr  
 305 310 315 320

Asp Leu Pro His His Thr Ile Val Phe Ala Lys Asp Tyr Thr Thr Asn  
 325 330 335

Ile Arg Asn Ile Phe Asp Asn Lys Thr Leu Thr Asp Asp Phe Ser Phe  
 340 345 350

Tyr Val Gln Asn Ala Ser Ala Ser Asp Asp Ser Leu Ala Pro Ala Gly  
 355 360 365

Lys Ser Ala Leu Tyr Val Leu Val Pro Met Pro Asn Asn Asp Ser Gly  
 370 375 380

Leu Asp Trp Gln Ala His Cys Gln Asn Val Arg Glu Gln Val Leu Asp  
 385 390 395 400

Thr Leu Gly Ala Arg Leu Gly Leu Ser Asp Ile Arg Ala His Ile Glu  
 405 410 415

Cys Glu Lys Ile Ile Thr Pro Gln Thr Trp Glu Thr Asp Glu His Val  
 420 425 430

Tyr Lys Gly Ala Thr Phe Ser Leu Ser His Lys Phe Ser Gln Met Leu  
 435 440 445

Tyr Trp Arg Pro His Asn Arg Phe Glu Glu Leu Ala Asn Cys Tyr Leu  
 450 455 460

Val Gly Gly Gly Thr His Pro Gly Ser Gly Leu Pro Thr Ile Tyr Glu  
 465 470 475 480

Ser Ala Arg Ile Ser Ala Lys Leu Ile Ser Gln Lys His Arg Val Arg  
 485 490 495

Phe Lys Asp Ile Ala His Ser Ala Trp Leu Lys Lys Ala Lys Ala  
 500 505 510

<210> 23

<211> 1491

<212> DNA

<213> Methylomonas 16a

<400> 23

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gtcggcggca agctcaacat catgaccaaa gacggctTTA ccttcgatct ggggccgtcc      180
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gaattggggcg tcgagattcg tTtagatgcc gaggtgtcgg aaatccaaaa acaggacggc      780
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aaaatgcagc gTtcgagcc tagctgttcc ggccgtgtgc tgcacttggg cgtggacagg      960
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gatgcggtat tcaaaagcca tcgcctgtcg gacgatccga ccatttatct ggtcgcgccg    1080
tgcaagaccg accccgcca ggccggggcc ggctgcgaga tcatcaaat cctgccccat    1140
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cgggtgctgg tcaaactcga acgcatgggc ctgacggatt tacgccaaca catcgtgacc    1260
gaagaatact ggacgccgct ggatattcag gccaaatatt attcaaacca gggctcgatt    1320
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gaattatcca atctgtatTTT cgtcggcggc agcgtcaatc ccggcgggcg catgccgatg    1440
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<210> 24

<211> 497

<212> PRT

<213> Methylomonas 16a

<400> 24

Met Asn Ser Asn Asp Asn Gln Arg Val Ile Val Ile Gly Ala Gly Leu  
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20 25 30

Gln Leu Ile Glu Lys Asn Asp Lys Val Gly Gly Lys Leu Asn Ile Met  
35 40 45

Thr Lys Asp Gly Phe Thr Phe Asp Leu Gly Pro Ser Ile Leu Thr Met  
50 55 60

Pro His Ile Phe Glu Ala Leu Phe Thr Gly Ala Gly Lys Asn Met Ala  
65 70 75 80

Asp Tyr Val Gln Ile Gln Lys Val Glu Pro His Trp Arg Asn Phe Phe  
85 90 95

Glu Asp Gly Ser Val Ile Asp Leu Cys Glu Asp Ala Glu Thr Gln Arg  
100 105 110

Arg Glu Leu Asp Lys Leu Gly Pro Gly Thr Tyr Ala Gln Phe Gln Arg  
115 120 125

Phe Leu Asp Tyr Ser Lys Asn Leu Cys Thr Glu Thr Glu Ala Gly Tyr  
130 135 140

Phe Ala Lys Gly Leu Asp Gly Phe Trp Asp Leu Leu Lys Phe Tyr Gly  
145 150 155 160

Pro Leu Arg Ser Leu Leu Ser Phe Asp Val Phe Arg Ser Met Asp Gln  
165 170 175

Gly Val Arg Arg Phe Ile Ser Asp Pro Lys Leu Val Glu Ile Leu Asn  
180 185 190

Tyr Phe Ile Lys Tyr Val Gly Ser Ser Pro Tyr Asp Ala Pro Ala Leu  
195 200 205

Met Asn Leu Leu Pro Tyr Ile Gln Tyr His Tyr Gly Leu Trp Tyr Val  
210 215 220

Lys Gly Gly Met Tyr Gly Met Ala Gln Ala Met Glu Lys Leu Ala Val  
225 230 235 240

Glu Leu Gly Val Glu Ile Arg Leu Asp Ala Glu Val Ser Glu Ile Gln  
245 250 255

Lys Gln Asp Gly Arg Ala Cys Ala Val Lys Leu Ala Asn Gly Asp Val  
260 265 270

Leu Pro Ala Asp Ile Val Val Ser Asn Met Glu Val Ile Pro Ala Met  
275 280 285

Glu Lys Leu Leu Arg Ser Pro Ala Ser Glu Leu Lys Lys Met Gln Arg  
290 295 300

Phe Glu Pro Ser Cys Ser Gly Leu Val Leu His Leu Gly Val Asp Arg  
305 310 315 320

Leu Tyr Pro Gln Leu Ala His His Asn Phe Phe Tyr Ser Asp His Pro  
325 330 335

Arg Glu His Phe Asp Ala Val Phe Lys Ser His Arg Leu Ser Asp Asp  
340 345 350

Pro Thr Ile Tyr Leu Val Ala Pro Cys Lys Thr Asp Pro Ala Gln Ala  
355 360 365

Pro Ala Gly Cys Glu Ile Ile Lys Ile Leu Pro His Ile Pro His Leu  
370 375 380

Asp Pro Asp Lys Leu Leu Thr Ala Glu Asp Tyr Ser Ala Leu Arg Glu  
385 390 395 400

Arg Val Leu Val Lys Leu Glu Arg Met Gly Leu Thr Asp Leu Arg Gln  
405 410 415

His Ile Val Thr Glu Glu Tyr Trp Thr Pro Leu Asp Ile Gln Ala Lys  
420 425 430

Tyr Tyr Ser Asn Gln Gly Ser Ile Tyr Gly Val Val Ala Asp Arg Phe  
435 440 445

Lys Asn Leu Gly Phe Lys Ala Pro Gln Arg Ser Ser Glu Leu Ser Asn  
450 455 460

Leu Tyr Phe Val Gly Gly Ser Val Asn Pro Gly Gly Gly Met Pro Met  
 465 470 475 480

Val Thr Leu Ser Gly Gln Leu Val Arg Asp Lys Ile Val Ala Asp Leu  
 485 490 495

Gln

<210> 25

<211> 912

<212> DNA

<213> Pantoea stewartii

<400> 25

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ggtgccgcga tgcgtgaagg cacgctggca ccgggcaaac gtattcgtcc gatgctgctg	180
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gatgcgcaga tgcgtcgggg gcgtcccacc attcacacgc agtacggtga acatgtggcg	360
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gtcgaagaac gcctgcgaca gcatttgccg ctggccagtg aacacctttc cgcggcatgc	840
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gccgtcagtt aa	912

<210> 26

<211> 303

<212> PRT

<213> Pantoea stewartii

<400> 26

Leu Thr Val Cys Ala Lys Lys His Val His Leu Thr Gly Ile Ser Ala  
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Glu Gln Leu Leu Ala Asp Ile Asp Ser Arg Leu Asp Gln Leu Leu Pro  
20 25 30

Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr  
35 40 45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Leu Thr Ala  
50 55 60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala  
65 70 75 80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met  
85 90 95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His  
100 105 110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu  
115 120 125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile  
130 135 140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln  
145 150 155 160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro  
165 170 175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr  
180 185 190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser  
195 200 205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln  
210 215 220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly  
225 230 235 240



Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu  
245 250 255

Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala  
260 265 270

Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln  
275 280 285

Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser  
290 295 300

<210> 27

<211> 1296

<212> DNA

<213> Pantoea stewartii

<400> 27

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aaagcgctgg taacgggcag cgatatcgga ttccagaccg tcggactgca aacgcacct	180
cccggttcct tatcgcacct gctgcacctg gccgcgcacc cactcggacc ctcgatgtta	240
cgactgatca atgaaatggc acgtaccagc gatatgcttt gccgggaact gcccgccgct	300
tttcatgcgt tgcagataga gggcgtgacg gttgatcaaa tggagccggc aggtgcagta	360
gtcgcagaag cgtcaggtct gccgtttgtt tcgggtggcct gcgcgctgcc gctcaaccgc	420
gaaccggggt tgcctctggc ggtgatgcct ttcgagtacg gcaccagcga tgcggctcgg	480
gaacgctata ccaccagcga aaaaatttat gactggctga tgcgacgtca cgatcgtgtg	540
atcgcgcacg atgcatgcag aatgggttta gcccgcgctg aaaaactgca tcattgtttt	600
tctccactgg cacaaatcag ccagttgatc cccgaactgg attttccccg caaagcgctg	660
ccagactgct ttcatgcggt tggaccgtta cggcaacccc aggggacgcc ggggtcatca	720
acttcttatt ttccgtcccc ggacaaaccc cgtatTTTTg cctcgctggg caccctgcag	780
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ctgctgacta acaccgatta cccgcagcgt atgacaaaaa ttcaggccgc attgcgtctg 1200  
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<210> 28

<211> 431

<212> PRT

<213> Pantoea stewartii

<400> 28

Met Ser His Phe Ala Val Ile Ala Pro Pro Phe Phe Ser His Val Arg  
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Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp  
35 40 45

Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu  
50 55 60

Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu  
65 70 75 80

Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu  
85 90 95

Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp  
100 105 110

Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro  
115 120 125

Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu  
130 135 140

Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg  
145 150 155 160

Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg  
165 170 175

His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro  
180 185 190

Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln  
195 200 205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe  
210 215 220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser  
225 230 235 240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu  
245 250 255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys  
260 265 270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly  
275 280 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln  
290 295 300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu  
305 310 315 320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser  
325 330 335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val  
340 345 350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe  
355 360 365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn  
370 375 380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu  
385 390 395 400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg  
405 410 415

Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu  
420 425 430

<210> 29

<211> 1149

<212> DNA

<213> *Pantoea stewartii*

<400> 29

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gcgggagggga accatacctg gtcctttcac gaagaggatt taacgctgaa tcagcatcgc 180  
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tacacgctg attctgcact acgcgtagga ttccaggcat ttatcgggtca ggagtggcaa 480  
ctgagcgcg cgcattggtt atcgtcaccg attatcatgg atgcgacggg cgatcagcaa 540  
aatggctacc gctttgttta taccctgccg ctttccgcaa ccgcaactgct gatcgaagac 600  
acacactaca ttgacaaggc taatcttcag gccgaacggg cgcgtcagaa cattcgcgat 660  
tatgtgcgc gacaggggtt gccgttacag acgttgctgc gggaagaaca ggggtgcattg 720  
cccattacgt taacggggcg taatcgtcag ttttggcaac agcaaccgca agcctgtagc 780  
ggattacgcg cggggctggt tcatccgaca accggctact ccctaccgct cgcggtgggg 840  
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gctcactttg cccagcaacg ttggcagcaa caggggtttt tccgcatgct gaatcgcattg 960  
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cccaggatt tgattgcccg cttttatgcy ggaaaactca ccgtgaccga tcggctacgc 1080  
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<210> 30

<211> 382

<212> PRT

<213> *Pantoea stewartii*

<400> 30

Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu Ala Asn  
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Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile  
20 25 30

Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser  
35 40 45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro  
50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg  
65 70 75 80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe  
85 90 95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr  
100 105 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg  
115 120 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp  
130 135 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln  
145 150 155 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr  
165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser  
180 185 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn  
195 200 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg  
210 215 220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu  
225 230 235 240

Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro  
245 250 255

Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly  
 260 265 270

Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu  
 275 280 285

Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala  
 290 295 300

Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met  
 305 310 315 320

Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg  
 325 330 335

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys  
 340 345 350

Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val  
 355 360 365

Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg  
 370 375 380

<210> 31

<211> 1479

<212> DNA

<213> Pantoea stewartii

<400> 31  
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 agcgcgattg aagaactggt tgcctctggcc ggtaaacagc ttaaggatta cgtcgagctg 240  
 ttgccggtca cgccgtttta tcgcctgtgc tgggagtcgg gcaaggtctt caattacgat 300  
 aacgaccagg cccagttaga agcgcagata cagcagttta atccgcgcga tgttgcgggg 360  
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tatacgcctga ttcacgcggtt agaacgggaa tggggcgctct ggtttccacg cggtggaacc 660  
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 gacggcagac ggtttgaaac ctgcgcggtg gcgtcgaacg ctgatgttgt acatacctat 840  
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 ccgttcgatt tccgcgacga gctcaatgcc tggcaagggtt cggccttctc ggttgaacct 1320  
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<210> 32

<211> 492

<212> PRT

<213> Pantoea stewartii

<400> 32

Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu  
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 20 25 30

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe  
 35 40 45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu  
 50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu  
 65 70 75 80

Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val  
85 90 95

Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln  
100 105 110

Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser  
115 120 125

Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe  
130 135 140

Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu  
145 150 155 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp  
165 170 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly  
180 185 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu  
195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val  
210 215 220

Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu  
225 230 235 240

Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala  
245 250 255

Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser  
260 265 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro  
275 280 285

Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn  
290 295 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu  
305 310 315 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His  
325 330 335



Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu  
 340 345 350

His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly  
 355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu  
 370 375 380

Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr  
 385 390 395 400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His  
 405 410 415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln  
 420 425 430

Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe  
 435 440 445

Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly  
 450 455 460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala  
 465 470 475 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile  
 485 490

<210> 33

<211> 891

<212> DNA

<213> Pantoea stewartii

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 aactgggct ttcattgccga ccagccctct tcgcagatgc ctgagcagcg cctgcagcag 180  
 cttgaaatga aaacgcgtca ggcctacgcc ggttcgcaaa tgcacgagcc cgcttttgcc 240  
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 gaagggttttg ccatggatgt gcgcgaaacg cgctacctga cactggacga tacgtctgct 360  
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gataacgcca cgctcgatcg cgctgcgat ctccgggtgg ctttccagtt gaccaacatt 480  
 gcgcgtgata ttgtcgacga tgcctcaggtg ggccgctgtt atctgcctga aagctggctg 540  
 gaagaggaag gactgacgaa agcgaattat gctgcgccag aaaaccggca ggccttaagc 600  
 cgtatcgccg ggcgactggg acgggaagcg gaaccctatt acgtatcatc aatggccggt 660  
 ctggcacaat tacccttacg ctccggcctgg gccatcgca cagcgaagca ggtgtaccgt 720  
 aaaattggcg tgaaagttga acaggccggt aagcaggcct gggatcatcg ccagtccacg 780  
 tccaccgccg aaaaattaac gcttttctg acggcatccg gtcaggcagt tacttcccgg 840  
 atgaagacgt atccaccccg tctgtctcat ctctggcagc gcccgatcta g 891

<210> 34

<211> 296

<212> PRT

<213> Pantoea stewartii

<400> 34

Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp  
1 5 10 15

Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His  
20 25 30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln  
35 40 45

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys  
50 55 60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala  
65 70 75 80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala  
85 90 95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr  
100 105 110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val  
115 120 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr  
130 135 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile  
145 150 155 160

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro  
165 170 175

Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala  
180 185 190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg  
195 200 205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu  
210 215 220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg  
225 230 235 240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His  
245 250 255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala  
260 265 270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro  
275 280 285

Ala His Leu Trp Gln Arg Pro Ile  
290 295

<210> 35

<211> 528

<212> DNA

<213> Pantoea stewartii

<400> 35

atgttgtgga tttggaatgc cctgatcgtg tttgtcaccg tggtcggcat ggaagtgggt	60
gctgcactgg cacataaata catcatgcac ggctgggggt ggggctggca tctttcacat	120
catgaaccgc gtaaaggcgc atttgaagtt aacgatctct atgccgtggt attcgccatt	180
gtgtcgattg ccctgattta cttcggcagt acaggaatct ggccgctcca gtggattggt	240
gcaggcatga ccgcttatgg tttactgtat tttatgggtcc acgacggact ggtacaccag	300
cgctggccgt tccgctacat accgcgcaaa ggctacctga aacggttata catggcccac	360

cgtatgcac atgctgtaag gggaaaagag ggctgcgtgt cctttggttt tctgtacgcg 420  
ccaccgttat ctaaacttca ggcgacgctg agagaaaaggc atcgggcctag atcgggcgct 480  
gccagagatg agcaggacgg ggtggatacg tcttcatccg ggaagtaa 528

<210> 36

<211> 175

<212> PRT

<213> Pantoea stewartii

<400> 36

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly  
1 5 10 15

Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp  
20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe  
35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala  
50 55 60

Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly  
65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly  
85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr  
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly  
115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser  
130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala  
145 150 155 160

Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys  
165 170 175

<210> 37

<211> 1599

<212> DNA

<213> Rhodococcus erythropolis AN12

<400> 37

gtgagcgcac ttctcgacgc cgctcgctgc ggttcgggac acaacgcgct cgtttcggcc 60  
gcgtatctcg cacgtgaggg ttggtcgggc gaggttctcg agaaggacac ggttctcggc 120  
ggtgccgtct cgaccgtcga gcgatttccc ggatacaagg tggaccgggg gtcgtctgcg 180  
cacctcatga tccgacacag tggcatcatc gaggaactcg gactcggcgc gcacggcctt 240  
cgctacatcg actgtgaccc gtgggcgttc gctccgcccg cccctggcac cgacggggcg 300  
ggcatcgtgt ttcacgcga cctcgatgca acctgccagt ccatcgaacg agcttgccgg 360  
acaaaggacg ccgacgcgta ccggcggttc gtcgcggtct ggtcggagcg cagccgacac 420  
gtgatgaagg cattttccac accgcccacc ggatcgaacc tgatcgggtc gttcggagga 480  
ctggccacag cgcgcggcaa cagcgaactg tcgcggcagt tcctcgcgcc gggcgacgca 540  
ctgctggacg agtatttcga cagtgaggca ctcaaggcag cgttggcggt gttcggcgcc 600  
cagtcggggc ctccgatgtc ggaaccggga accgctccga tggtcggcct cgcgggccctc 660  
atgcacgtcc tgccgcccgg gcgagcagtc ggagggagcg gcgcactgag tgctgcgttg 720  
gcatcccgga tggctgtcga cggcgccacc gtcgcgctcg gtgacggcgt gacgtcgatc 780  
cgccggaact cgaatcactg gaccgtcaca accgagagcg gtcgagaagt tcacgtcgcg 840  
aaggtaatcg cgggttgcca catcctcacg aactcgcgtc tcctgggcaa cggaggcttc 900  
gaccgaacca cgctcgatca ctggcgggcg aagatcaggg tcggccccgg catcggcgct 960  
gtattgcgac tggcgacatc tgcgtccccg tcctaccgcg gcgacgccac gacacgggaa 1020  
agtacctcgg gattgcaatt actcgtttcc gatcgcgccc atttgcgcac tgcacacggc 1080  
gcagcactgg caggggaact gcctcctcgc cctgcgggtc tcggaatgag tttcagcgga 1140  
atcgatccca cgatcgcccc ggccggggcg catcaggtga cactgtggtc gcagtggcag 1200  
ccgtatcgtc tcagcggaca tcgcgattgg gcgtcggtcg ccgaggccga ggccgaccgg 1260  
atcgtcggcg agatggaggc ttttgacccc ggattcaccg attccgtcct cgaccgcttc 1320  
attcaaactc cccgcgacat cgagtcggaa ttggggatga tcggcggaaa tgtcatgcac 1380  
gtcgagatgt cactcgatca gatgatgttg tggcgaccgc ttcccgaact gtccggccat 1440  
cgcgttccgg gagcagacgg gttgtatctg accggagcct cgacgcaccc cgggtggtgg 1500  
gtgtccggag ccagtggtcg cagtgccgct cgaatcgcac tgtccgacag ccgccgggg 1560  
aaagcagatc agtggatgcg tcgttcgagc aggtcgtga 1599

<210> 38

<211> 532

<212> PRT

<213> Rhodococcus erythropolis AN12

<400> 38

Met Ser Ala Phe Leu Asp Ala Val Val Val Gly Ser Gly His Asn Ala  
1 5 10 15

Leu Val Ser Ala Ala Tyr Leu Ala Arg Glu Gly Trp Ser Val Glu Val  
20 25 30

Leu Glu Lys Asp Thr Val Leu Gly Gly Ala Val Ser Thr Val Glu Arg  
35 40 45

Phe Pro Gly Tyr Lys Val Asp Arg Gly Ser Ser Ala His Leu Met Ile  
50 55 60

Arg His Ser Gly Ile Ile Glu Glu Leu Gly Leu Gly Ala His Gly Leu  
65 70 75 80

Arg Tyr Ile Asp Cys Asp Pro Trp Ala Phe Ala Pro Pro Ala Pro Gly  
85 90 95

Thr Asp Gly Pro Gly Ile Val Phe His Arg Asp Leu Asp Ala Thr Cys  
100 105 110

Gln Ser Ile Glu Arg Ala Cys Gly Thr Lys Asp Ala Asp Ala Tyr Arg  
115 120 125

Arg Phe Val Ala Val Trp Ser Glu Arg Ser Arg His Val Met Lys Ala  
130 135 140

Phe Ser Thr Pro Pro Thr Gly Ser Asn Leu Ile Gly Ala Phe Gly Gly  
145 150 155 160

Leu Ala Thr Ala Arg Gly Asn Ser Glu Leu Ser Arg Gln Phe Leu Ala  
165 170 175

Pro Gly Asp Ala Leu Leu Asp Glu Tyr Phe Asp Ser Glu Ala Leu Lys  
180 185 190

Ala Ala Leu Ala Trp Phe Gly Ala Gln Ser Gly Pro Pro Met Ser Glu  
195 200 205

Pro Gly Thr Ala Pro Met Val Gly Phe Ala Ala Leu Met His Val Leu  
210 215 220

Pro Pro Gly Arg Ala Val Gly Gly Ser Gly Ala Leu Ser Ala Ala Leu  
225 230 235 240

Ala Ser Arg Met Ala Val Asp Gly Ala Thr Val Ala Leu Gly Asp Gly  
245 250 255

Val Thr Ser Ile Arg Arg Asn Ser Asn His Trp Thr Val Thr Thr Glu  
260 265 270

Ser Gly Arg Glu Val His Ala Arg Lys Val Ile Ala Gly Cys His Ile  
275 280 285

Leu Thr Thr Leu Asp Leu Leu Gly Asn Gly Gly Phe Asp Arg Thr Thr  
290 295 300

Leu Asp His Trp Arg Arg Lys Ile Arg Val Gly Pro Gly Ile Gly Ala  
305 310 315 320

Val Leu Arg Leu Ala Thr Ser Ala Leu Pro Ser Tyr Arg Gly Asp Ala  
325 330 335

Thr Thr Arg Glu Ser Thr Ser Gly Leu Gln Leu Leu Val Ser Asp Arg  
340 345 350

Ala His Leu Arg Thr Ala His Gly Ala Ala Leu Ala Gly Glu Leu Pro  
355 360 365

Pro Arg Pro Ala Val Leu Gly Met Ser Phe Ser Gly Ile Asp Pro Thr  
370 375 380

Ile Ala Pro Ala Gly Arg His Gln Val Thr Leu Trp Ser Gln Trp Gln  
385 390 395 400

Pro Tyr Arg Leu Ser Gly His Arg Asp Trp Ala Ser Val Ala Glu Ala  
405 410 415

Glu Ala Asp Arg Ile Val Gly Glu Met Glu Ala Phe Ala Pro Gly Phe  
420 425 430

Thr Asp Ser Val Leu Asp Arg Phe Ile Gln Thr Pro Arg Asp Ile Glu  
435 440 445

Ser Glu Leu Gly Met Ile Gly Gly Asn Val Met His Val Glu Met Ser  
450 455 460

Leu Asp Gln Met Met Leu Trp Arg Pro Leu Pro Glu Leu Ser Gly His  
465 470 475 480

Arg Val Pro Gly Ala Asp Gly Leu Tyr Leu Thr Gly Ala Ser Thr His  
485 490 495

Pro Gly Gly Gly Val Ser Gly Ala Ser Gly Arg Ser Ala Ala Arg Ile  
500 505 510

Ala Leu Ser Asp Ser Arg Arg Gly Lys Ala Ser Gln Trp Met Arg Arg  
515 520 525

Ser Ser Arg Ser  
530

<210> 39

<211> 30

<212> DNA

<213> Methylomonas 16a

<400> 39

ccgagtactg aagcgggttt ttgcagggag

30

<210> 40

<211> 25

<212> DNA

<213> Methylomonas 16a

<400> 40

gggctagctg ctccgattgt tacag

25

<210> 41

<211> 38

<212> DNA

<213> Artificial Sequence

<400> 41

agcagctagc ggaggaataa accatgagcg catttctc

38



<210> 42

<211> 26

<212> DNA

<213> Artificial Sequence

<400> 42

gactagtcac gacctgctcg aacgac

26

<210> 43

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 43

atgacgggtct gcgcaaaaaa acacg

25

<210> 44

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 44

gagaaattat gttgtggatt tggaatgc

28

<210> 45

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 45  
gagtttgatc ctggctcag

19

<210> 46

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 46  
taccttggtta cgactt

16

<210> 47

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc\_feature

<222> (11)..(11)

<223> Y = C or T

<220>

<221> misc\_feature

<222> (12)..(12)

<223> M = A or C

<400> 47  
gtgccagcag ymgcgg

17

<210> 48

<211> 21

<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 48  
atgagcgcat ttctcgacgc c

21

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 49  
tcacgacctg ctogaacgac

20

<210> 50

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 50  
gagaattggc tgaaaaacca aataaataac aaaatttagc gagtaaattg

50

<210> 51

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 51  
ttcaattgac aggggggctc gttctgattt agagttgctg ccagcttttt

50

<210> 52

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 52  
gggttggtcca gatgttggtg agcggtcctt ataactataa ctgtaacaat

50

<210> 53

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 53  
ttaatggtct tgccatgaga tgtgctccga ttgttacagt tatagttata

50

<210> 54

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 54  
ccccctgtca attgaaagcc cgccatttac tcgttaaatt ttgttattta

50

<210> 55

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 55

aaggatccgc gtattcgtac tc

22

<210> 56

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 56

ctggatccga tctagaaata ggctcgagtt gtcgttcagg

40

<210> 57

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 57

aaggatccta ctcgagctga catcagtgc

30

<210> 58

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 58  
gctctagatg caaccagaat cg

22

<210> 59

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 59  
tggctcgaga gtaaaacact caag

24

<210> 60

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 60  
tagctcgagt cacgcttgc

19